Search Paper 5

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 NEWS  1          Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2  Sep 17  IMSworld Pharmaceutical Company Directory name change
                  to PHARMASEARCH
 NEWS  3  Oct 09  Korean abstracts now included in Derwent World Patents
                  Index
 NEWS  4  Oct 09  Number of Derwent World Patents Index updates increased
 NEWS  5  Oct 15  Calculated properties now in the REGISTRY/ZREGISTRY File
 NEWS  6  Oct 22  Over 1 million reactions added to CASREACT
 NEWS  7  Oct 22  DGENE GETSIM has been improved
 NEWS  8  Oct 29  AAASD no longer available
 NEWS  9  Nov 19  New Search Capabilities  USPATFULL and USPAT2
 NEWS 10  Nov 19  TOXCENTER(SM) - new toxicology file now available on STN
 NEWS 11  Nov 29  COPPERLIT now available on STN
 NEWS 12  Nov 29  DWPI revisions to NTIS and US Provisional Numbers
 NEWS 13  Nov 30  Files VETU and VETB to have open access
 NEWS 14  Dec 10  WPINDEX/WPIDS/WPIX New and Revised Manual Codes for 2002
 NEWS 15  Dec 10  DGENE BLAST Homology Search
 NEWS 16  Dec 17  WELDASEARCH now available on STN
 NEWS 17  Dec 17  STANDARDS now available on STN
 NEWS 18  Dec 17  New fields for DPCI
 NEWS 19  Dec 19  CAS Roles modified
 NEWS 20  Dec 19  1907-1946 data and page images added to CA and CAplus
 NEWS 21  Jan 25  BLAST(R) searching in REGISTRY available in STN on the Web
 NEWS 22  Jan 25  Searching with the P indicator for Preparations
 NEWS 23  Jan 29  FSTA has been reloaded and moves to weekly updates
 NEWS 24  Feb 01  DKILIT now produced by FIZ Karlsruhe and has a new update
                  frequency

 NEWS EXPRESS  February 1 CURRENT WINDOWS VERSION IS V6.0d,
               CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP),
               AND CURRENT DISCOVER FILE IS DATED 05 FEBRUARY 2002
 NEWS HOURS    STN Operating Hours Plus Help Desk Availability
 NEWS INTER    General Internet Information
 NEWS LOGIN    Welcome Banner and News Items
 NEWS PHONE    Direct Dial and Telecommunication Network Access to STN
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=> s oryzae and array
L1 6 ORYZAE AND ARRAY

=> duplicate remove l1
DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n
PROCESSING COMPLETED FOR L1
L2 6 DUPLICATE REMOVE L1 (0 DUPLICATES REMOVED)

=> d 1-6 bib ab

L2 ANSWER 1 OF 6 MEDLINE
AN 2002011481 MEDLINE
DN 21282285 PubMed ID: 11387980
TI Dissection of defence response pathways in rice.
AU Leach J E; Leung H; Wang G L
CS Department of Plant Pathology, 4024 Throckmorton Plant Sciences Center, Kansas State University, Manhattan, KS 66506-5502, USA.
SO NOVARTIS FOUNDATION SYMPOSIUM, (2001) 236 190-200; discussion 200-4. Ref: 41
Journal code: 9807767.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 200112
ED Entered STN: 20020121
Last Updated on STN: 20020121
Entered Medline: 20011204
AB The cloning of major resistance genes has led to a better understanding of the molecular biology of the steps for induction of resistance, yet much remains to be discovered about the downstream genes that collectively confer resistance, i.e. the defence response (DR) genes. We are dissecting the pathways contributing to resistance in rice by identifying a collection of mutants with deletions or other structural rearrangements in DR genes. The collection of rice mutants has been screened for many characters, including increased susceptibility or resistance to Magnaporthe grisea and Xanthomonas **oryzae** pv. **oryzae**.
A collection of enhanced sequence tags (ESTs) and putative DR genes has been established to facilitate detection of mutants with deletions in DR genes. **Arrays** of DR genes will be used to create gene expression profiles of interesting mutants. Successful application of the mutant screen will have broad utility in identifying candidate genes involved in disease response and other metabolic pathways.

L2 ANSWER 2 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1999:308754 BIOSIS
DN PREV199900308754
TI The rumen ecosystem: As a fountain source of nobel enzymes: Review.
AU Lee, S. S. (1); Shin, K. J.; Kim, W. Y.; Ha, J. K.; Han, In K.
CS (1) Nutritional Physiology Division, National Livestock Research Institute, RDA, Suweon, 441-350 South Korea
SO Asian-Australasian Journal of Animal Sciences, (Sept., 1999) Vol. 12, No. 6, pp. 988-1001.
ISSN: 1011-2367.
DT General Review
LA English
SL English
AB The rumen ecosystem is increasingly being recognized as a promising source of superior polysaccharide-degrading enzymes. They contain a wide **array** of novel enzymes at the levels of specific activities of 1,184, 1,069, 119, 390, 327 and 946 mumol reducing sugar released/min/mg protein for endoglucanase, xylanase, polygalactouronase, amylase, glucanase and arabinase, respectively. These enzymes are mainly located in the surface of rumen microbes. However, glycoside-degrading enzymes (e.g. glucosidase, fucosidase, xylosidase and arabinofuranosidase, etc.) are mainly located in the rumen fluid, when detected enzyme activities according to the ruminal compartments (e.g. enzymes in whole rumen

contents, feed-associated [redacted]ymes, microbial cell-associate[redacted]nzymes, and enzymes in the rumen fluid). Ruminal fungi are the primary contributors to high production of novel enzymes; the bacteria and protozoa also have important functions, but less central roles. The enzyme activities of bacteria, protozoa and fungi were detected 32.26, 19.21 and 47.60 mol glucose released/min/mL medium for cellulase; 42.56, 14.96 and 64.93 mmol xylose released/min/mL medium after 48h incubation, respectively. The polysachharide-degrading enzyme activity of ruminal anaerobic fungi (e.g. Neocallimastix patriciarum and Piromyces communis, etc.) was much higher approximately 3apprx6 times than that of aerobic fungi (e.g. Tricoderma reesei, T. viridae and Aspergillus **oryzae**, etc.) used widely in industrial process. Therefore, the rumen ecosystem could be a growing source of novel enzymes having a tremendous potential for industrial applications.

L2 ANSWER 3 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1997:389735 BIOSIS
DN PREV199799688938
TI Acoustic counting of adult insects with differing rates and intensities of sound production in stored wheat.
AU Mankin, R. W.; Shuman, D.; Coffelt, J. A.
CS USDA-ARS Cent. Med. Agric. Vet. Entomol., Gainesville, FL 32604 USA
SO Journal of Economic Entomology, (1997) Vol. 90, No. 4, pp. 1032-1038. ISSN: 0022-0493.
DT Article
LA English
AB Automated acoustic detection systems count the insects in a grain sample by analyzing the spatial and temporal distribution of sounds. The acoustic location fixing insect detector is an automated system developed originally to quantify hidden larval infestations in 1-kg samples of wheat. The detector analyzes input from an **array** of sensors embedded in the sample container walls. It identifies (scores) a specific pattern of input as an insect if the spatial and temporal distribution matches the criteria based on a calibration with 4th-instar rice weevil, Sitophilus **oryzae** (L). However, expanded testing has revealed considerable differences in the spatial and temporal distributions of sounds made by insects of different species and sizes. These differences were examined in a series of tests with insects that range an order of magnitude above and below the 1.5-mg weight of the S. **oryzae** larvae. A particular focus was the detection order of the first 2 sensors registering each sound. Multiple sounds from an insect tend to cluster together into a small number of contiguous 1st:2nd sensor detection pairs, but the pattern for background noises is random. It was determined that the cluster size, the number of contiguous 1st:2nd detection pairs, was proportional to insect weight. The rate of sound detection was inversely proportional to weight. Thus, to reliably count insects with widely varying sound production patterns, the sound pattern identification algorithm needs to self correct, depending on the input received from the grain sample. Adults or larvae generating large numbers of loud sounds, typically weighing gt 1 mg, can be scored in a few seconds, but those generating small numbers of weak sounds, typically lt 1 mg, should be monitored for periods gt 10 min. The possibility of using differences in cluster size to distinguish among species is also discussed.

L2 ANSWER 4 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1993:341813 BIOSIS
DN PREV199396039812
TI Quantitative acoustical detection of larvae feeding inside kernels of grain.
AU Shuman, Dennis; Coffelt, James A.; Vick, Kenneth W.; Mankin, Richard W.
CS Insect Attractants Behav. Basic Biol. Res. Lab., USDA ARS, Gainesville, FL 32604 USA
SO Journal of Economic Entomology, (1993) Vol. 86, No. 3, pp. 933-938. ISSN: 0022-0493.
DT Article
LA English
AB An automated, computer-based electronic acoustic system was developed to quantify infestation of internally feeding larvae in a grain sample using spatial localization of insects in the sample. Localization was determined using arrival times of sounds produced by insect feeding activity as

received by an **array** of acoustic transducers. In a test conducted with 0-3 fourth instars of the rice weevil, Sitophilus **oryzae** (L.), in 1-kg samples of wheat, the system overassessed the number of larvae present in 6% of the trials and underassessed the number of larvae present in 34% of the trials. When Federal Grain Inspection Service (FGIS) standards were applied in evaluating performance, the system was 92% accurate in grading "clean" grain and 64% accurate in grading "infested" grain.

L2 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1993:361420 BIOSIS
DN PREV199396047095
TI Forage quality, mineral constituents, and performance of beef yearlings grazing two crested wheatgrasses.
AU Vogel, K. P. (1); Gabrielsen, B. C.; Ward, J. K.; Anderson, B. E.; Mayland, H. F.; Masters, R. A.
CS (1) USDA-ARS, Dep. Agron., Univ. Nebr., Lincoln, NE 68583 USA
SO Agronomy Journal, (1993) Vol. 85, No. 3, pp. 584-590.
ISSN: 0002-1962.
DT Article
LA English
AB In the central Great Plains, crested wheatgrasses (Agropyron cristatum (L.) Gaetner and A. desertorum (Fischer ex Link) Schultes) are best utilized for early spring and late fall grazing. The principal objective of this study was to determine if beef (Bos taurus L.) yearlings grazing 'Ruff' (A. cristatum) during the spring grazing season had higher average daily gains and gains per hectare than cattle grazing 'Nordan' (A. desertorum). These cultivars were evaluated in grazing trials (four replications) in eastern Nebraska (USA) in 1985, 1986, and 1987. The 0.8-ha pastures were seeded in the fall of 1983 on a Typic Argiudoll soil and were fertilized annually with 68 to 90 kg N ha-1. Grazing was for 6 wk each spring by yearling steers with a beginning average weight of 250 kg. Averaged over 3 yr, Ruff produced higher gains per hectare than Nordan (272 vs 245 kg ha-1) probably because it produced more herbage because of its better persistence. At the end of the trial, the average basal cover of Ruff and Nordan were 21 and 6%, respectively. Three-year mean average daily gains were Ruff = 1.28 vs. Nordan = 1.34 kg d-1, which were unexpected, because Ruff generally had higher forage quality as measured by an **array** of parameters. Ruff forage had a higher, less desirable grass tetany ratio ((K/ (Mg + Ca)) than Nordan (2.6 vs. 2.3) averaged over 3 yr. Cattle grazing Ruff had lower blood serum Mg levels than cattle grazing Nordan (15.4 vs. 16.2 mg L-1), both of which were below the hypomagnesemia threshold of 18 mg L-1. This condition may have reduced intake and animal gains. These results indicate the need for evaluating pasture and range grass cultivars under grazing conditions.

L2 ANSWER 6 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1991:344865 BIOSIS
DN BA92:44240
TI SYNTHETIC AND MECHANISTIC STUDIES ON FUNGAL METABOLIC PATHWAYS A GUIDE TO FUNGICIDE DESIGN.
AU SIMPSON T J; DILLON M P; DONOVAN T M
CS SCH. CHEM., UNIVERSITY BRISTOL, BRISTOL BS8 1TS, UK.
SO PESTIC SCI, (1991) 31 (4), 539-554.
CODEN: PSSCBG. ISSN: 0031-613X.
FS BA; OLD
LA English
AB The polyketide biosynthetic pathway is responsible for the formation in microorganisms and plants of a vast **array** of diverse structures, many of which display important biological activity. A brief overview of the pathway, with emphasis on present problems and future developments, is presented and the impact of genetics on chemical and biochemical studies of polyketide biosynthesis is highlighted. Biosynthetic and mechanistic studies on three pathways are described, to illustrate how these studies may provide an insight into the mode of action of particular compounds, or how particular pathways may be inhibited. LL-D253.alpha. is an antibiotic chromosome produced by a number of Phoma species. Stable isotope labelling studies have indicated the involvement of cyclopropylcyclohexadienyl intermediates in the formation of the hydroxyethyl side chain indicating a possible mode of action. Similar studies of monocerin indicate the

involvement of quinone met[redacted]e intermediates. A synthesis o[redacted]monocerin, modelled on the biosynthesis pathway, is described. Scytalone and vermelone are intermediates on the pathway to melanin in certain pathogenic fungi, e.g. Pyricularia **oryzae**. Progress with biosynthetic studies on this pathway is described.

=> s aspergillus oryzae and array
L3 2 ASPERGILLUS ORYZAE AND ARRAY

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PROCESSING COMPLETED FOR L3
L4 2 DUPLICATE REMOVE L3 (0 DUPLICATES REMOVED)

=> d 1-2 bib ab

L4 ANSWER 1 OF 2 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1999:308754 BIOSIS
DN PREV199900308754
TI The rumen ecosystem: As a fountain source of nobel enzymes: Review.
AU Lee, S. S. (1); Shin, K. J.; Kim, W. Y.; Ha, J. K.; Han, In K.
CS (1) Nutritional Physiology Division, National Livestock Research Institute, RDA, Suweon, 441-350 South Korea
SO Asian-Australasian Journal of Animal Sciences, (Sept., 1999) Vol. 12, No. 6, pp. 988-1001.
ISSN: 1011-2367.
DT General Review
LA English
SL English
AB The rumen ecosystem is increasingly being recognized as a promising source of superior polysaccharide-degrading enzymes. They contain a wide **array** of novel enzymes at the levels of specific activities of 1,184, 1,069, 119, 390, 327 and 946 mumol reducing sugar released/min/mg protein for endoglucanase, xylanase, polygalactouronase, amylase, glucanase and arabinase, respectively. These enzymes are mainly located in the surface of rumen microbes. However, glycoside-degrading enzymes (e.g. glucosidase, fucosidase, xylosidase and arabinofuranosidase, etc.) are mainly located in the rumen fluid, when detected enzyme activities according to the ruminal compartments (e.g. enzymes in whole rumen contents, feed-associated enzymes, microbial cell-associated enzymes, and enzymes in the rumen fluid). Ruminal fungi are the primary contributors to high production of novel enzymes; the bacteria and protozoa also have important functions, but less central roles. The enzyme activities of bacteria, protozoa and fungi were detected 32.26, 19.21 and 47.60 mol glucose released/min/mL medium for cellulase; 42.56, 14.96 and 64.93 mmol xylose released/min/mL medium after 48h incubation, respectively. The polysachharide-degrading enzyme activity of ruminal anaerobic fungi (e.g. Neocallimastix patriciarum and Piromyces communis, etc.) was much higher approximately 3apprx6 times than that of aerobic fungi (e.g. Tricoderma reesei, T. viridae and **Aspergillus oryzae**, etc.) used widely in industrial process. Therefore, the rumen ecosystem could be a growing source of novel enzymes having a tremendous potential for industrial applications.

L4 ANSWER 2 OF 2 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1993:361420 BIOSIS
DN PREV199396047095
TI Forage quality, mineral constituents, and performance of beef yearlings grazing two crested wheatgrasses.
AU Vogel, K. P. (1); Gabrielsen, B. C.; Ward, J. K.; Anderson, B. E.; Mayland, H. F.; Masters, R. A.
CS (1) USDA-ARS, Dep. Agron., Univ. Nebr., Lincoln, NE 68583 USA
SO Agronomy Journal, (1993) Vol. 85, No. 3, pp. 584-590.
ISSN: 0002-1962.
DT Article
LA English
AB In the central Great Plains, crested wheatgrasses (Agropyron cristatum (L.) Gaetner and A. desertorum (Fischer ex Link) Schultes) are best utilized for early spring and late fall grazing. The principal objective of this study was to determine if beef (Bos taurus L.) yearlings grazing

'Ruff' (A. cristatum) dur[redacted] the spring grazing season had [redacted]gher average daily gains and gains per hectare than cattle grazing 'Nordan' (A. desertorum). These cultivars were evaluated in grazing trials (four replications) in eastern Nebraska (USA) in 1985, 1986, and 1987. The 0.8-ha pastures were seeded in the fall of 1983 on a Typic Argiudoll soil and were fertilized annually with 68 to 90 kg N ha-1. Grazing was for 6 wk each spring by yearling steers with a beginning average weight of 250 kg. Averaged over 3 yr, Ruff produced higher gains per hectare than Nordan (272 vs 245 kg ha-1) probably because it produced more herbage because of its better persistence. At the end of the trial, the average basal cover of Ruff and Nordan were 21 and 6%, respectively. Three-year mean average daily gains were Ruff = 1.28 vs. Nordan = 1.34 kg d-1, which were unexpected, because Ruff generally had higher forage quality as measured by an **array** of parameters. Ruff forage had a higher, less desirable grass tetany ratio ((K/ (Mg + Ca)) than Nordan (2.6 vs. 2.3) averaged over 3 yr. Cattle grazing Ruff had lower blood serum Mg levels than cattle grazing Nordan (15.4 vs. 16.2 mg L-1), both of which were below the hypomagnesemia threshold of 18 mg L-1. This condition may have reduced intake and animal gains. These results indicate the need for evaluating pasture and range grass cultivars under grazing conditions.

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=> s aspergillus oryzae and (gene or sequence or cDNA)
L5          660 ASPERGILLUS ORYZAE AND (GENE OR SEQUENCE OR CDNA)

=> s aspergillus oryzae and review
L6           24 ASPERGILLUS ORYZAE AND REVIEW

=> s l6 and py<1998
L7           17 L6 AND PY<1998

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DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE?  Y/(N):n
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L8            16 DUPLICATE REMOVE L7 (1 DUPLICATE REMOVED)

=> d 1-10 bib ab

L8   ANSWER 1 OF 16     MEDLINE
AN   97444510     MEDLINE
DN   97444510   PubMed ID: 9299700
TI   Expression cloning of fungal enzyme genes; a novel approach for efficient
     isolation of enzyme genes of industrial relevance.
AU   Dalboge H
CS   Enzyme Business. Novo Nordisk AIS, Bagsvard, Denmark.. hda@novo.dk
SO   FEMS MICROBIOLOGY REVIEWS, (1997 Aug) 21 (1) 29-42.  Ref: 21
     Journal code: AO4; 8902526. ISSN: 0168-6445.
CY   Netherlands
DT   Journal; Article; (JOURNAL ARTICLE)
     General Review; (REVIEW)
     (REVIEW, TUTORIAL)
LA   English
FS   Priority Journals
EM   199710
ED   Entered STN: 19971013
     Last Updated on STN: 19971013
     Entered Medline: 19971001
AB   Expression cloning is a relatively new method for fast and efficient
     cloning of enzyme genes from fungi that are known to make complex enzyme
     mixtures. In contrast to traditional cloning methods that are usually
     dependent on knowledge of at least a partial amino acid sequence in order
     to synthesize appropriate DNA probes or primers, the expression cloning
     method solely relies on access to reliable and sensitive enzyme assays. A
     representative expression cDNA library is made in Saccharomyces cerevisiae
     form the donor strain and relevant cDNA clones are detected directly based
     on the encoded enzyme activity. Thus, time-consuming enzyme purification
     and characterization steps are avoided. The method has been applied on the
     characterization of extracellular enzyme genes from the filamentous fungus
     Aspergillus aculeatus and has resulted in the isolation of 20 different
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enzyme genes such as endo-[redacted]canases, xylanases, pectinases[redacted]roteases, hemicellulases and rhamnogalacturonan-degrading enzymes. All enzymes have been expressed in **Aspergillus oryzae**, purified and characterized. In the present **review** a description of the expression cloning technique will be given as well as examples of how the technique has been used in the exploration and characterization of a commercial enzyme product that is known to consist of a complex mixture of more than 25 different enzyme activities.

L8 ANSWER 2 OF 16 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1995:550288 BIOSIS
DN PREV199698564588
TI Influence of direct-fed microbials on ruminal microbial fermentation and performance of ruminants: A **review**.
AU Yoon, I. K.; Stern, M. D. (1)
CS (1) Dep. Animal Sci., Univ. Minnesota, St. Paul, MN 55108 USA
SO Asian-Australasian Journal of Animal Sciences, (1995) Vol. 8, No. 6, pp. 533-555.
ISSN: 1011-2367.
DT General Review
LA English
AB Direct-fed microbials (DFM) have been used to enhance milk production in lactating cattle and to increase feed efficiency and body weight gain in growing ruminants. Primary microorganisms that have been used as DFM for ruminants are fungal cultures including Aspergillus otyzae and Saccharomyces cerevisiae and lactic acid bacteria such as Lactobacillus or Streptococcus. Attempts have been made to determine the basic mechanisms describing beneficial effects of DFM supplements. Various modes of action for DFM have been suggested including : stimulation of ruminal microbial growth, stabilization of ruminal pH, changes in ruminal microbial fermentation pattern, increases in digestibility of nutrients ingested, greater nutrient flow to the small intestine, greater nutrient retention and alleviation of stress, however, these responses have not been observed consistently. Variations in microbial supplements, dosage level, production level and age of the animal, diet and environmental condition or various combinations of the above may partially explain the inconsistencies in response. This **review** summarizes production responses that have been observed under various conditions with supplemental DFM and also corresponding modification of ruminal fermentation and other changes in the gastrointestinal tract of ruminant animals.

L8 ANSWER 3 OF 16 MEDLINE DUPLICATE 1
AN 92239105 MEDLINE
DN 92239105 PubMed ID: 1368061
TI On the safety of **Aspergillus oryzae**: a **review**
.
AU Barbesgaard P; Heldt-Hansen H P; Diderichsen B
CS Novo Nordisk A/S, Bagsvaerd, Denmark.
SO APPLIED MICROBIOLOGY AND BIOTECHNOLOGY, **(1992 Feb)** 36 (5) 569-72. Ref: 43
Journal code: AMC; 8406612. ISSN: 0175-7598.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS B
EM 199206
ED Entered STN: 19950809
Last Updated on STN: 19950809
Entered Medline: 19920601

L8 ANSWER 4 OF 16 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1992:531748 BIOSIS
DN BR43:117448
TI TECHNIQUES FOR THE ESTIMATION OF CELL CONCENTRATIONS IN THE PRESENCE OF SUSPENDED SOLIDS.
AU KENNEDY M J; THAKUR M S; WANG D I C; STEPHANOPOULOS G N
CS NEW ZEALAND INST. INDUSTRIAL RES. AND DEV., BOX 31-310, LOWER HUTT, NEW

ZEALAND.
SO Biotechnol. Prog., (1992) 8 (5), 375-381.
CODEN: BIPRET. ISSN: 8756-7938.
FS BR; OLD
LA English

L8 ANSWER 5 OF 16 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1991:395921 BIOSIS
DN BR41:57766
TI ENZYMATIC METHODS FOR THE PRODUCTION OF ITACONIC AND KOJIC ACIDS.
AU JURANYIOVA E; MATISOVA E
CS CHEMICKOTECHNOL. FAK. SVST, RADLINSKEHO 9, 812 37 BRATISLAVA, CSFR.
SO Biologia (Bratislava), (1991) 46 (4), 355-366.
CODEN: BLOAAO. ISSN: 0006-3088.
FS BR; OLD
LA Slovak

L8 ANSWER 6 OF 16 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1991:58947 BIOSIS
DN BR40:24302
TI ANTIFUNGAL AND SURGICAL TREATMENT OF INVASIVE ASPERGILLOSIS **REVIEW** OF 2121 PUBLISHED CASES.
AU DENNING D W; STEVENS D A
CS DIV. INFECTIOUS DISEASES, DEP. MEDICINE, SANTA CLARA VALLEY MEDICAL CENTER, 751 SOUTH BASCOM AVENUE, SAN JOSE, CALIF. 95128.
SO Rev. Infect. Dis., (1990) 12 (6), 1147-1201.
CODEN: RINDDG. ISSN: 0162-0886.
FS BR; OLD
LA English

L8 ANSWER 7 OF 16 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1990:385533 BIOSIS
DN BR39:56494
TI DISEASES OF SILKWORMS II. PEBRINE MYCOTIC DISEASES.
AU HARTWIG A; MIECZKOWSKI K
CS UL. KRYNICZNA 3/2, 03-934 WARSZAWA, POL.
SO Med. Weter., (1990) 46 (1-3), 21-23.
CODEN: MDWTAG. ISSN: 0025-8628.
FS BR; OLD
LA Polish

L8 ANSWER 8 OF 16 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1988:78167 BIOSIS
DN BR34:34686
TI FORMATION OF OLIGOSACCHARIDES DURING ENZYMATIC LACTOSE HYDROLYSIS AND THEIR IMPORTANCE IN A WHEY HYDROLYSIS PROCESS PART II EXPERIMENTAL.
AU PRENOSIL E S; BOURNE J R
CS SWISS FEDERAL INST. TECHNOL. ETH , CHEM. ENGINEERING DEP. TCL , CH-8092 ZURICH, SWITZERLAND.
SO Biotechnol. Bioeng., (1987) 30 (9), 1026-1031
CODEN: BIBIAU. ISSN: 0006-3592.
FS BR; OLD
LA English

L8 ANSWER 9 OF 16 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1988:280502 BIOSIS
DN BR35:8816
TI ALPHA AMYLASE TERTIARY STRUCTURES AND THEIR INTERACTIONS WITH POLYSACCHARIDES.
AU BUISSON G; DUEE E; PAYAN F; HASER R
CS CEA-CEN, DRF-G, LAB. DE BIOL. STRUCTURALE, 85X, 38041 GRENOBLE CEDEX, FR.
SO 2ND INTERNATIONAL WORKSHOP ON PLANT POLYSACCHARIDES, GRENOBLE, FRANCE, JULY 8-10. FOOD HYDROCOLLOIDS, (1987) 1 (5-6), 399-406.
CODEN: FOHYES.
FS BR; OLD
LA English

L8 ANSWER 10 OF 16 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
AN 1987:457207 BIOSIS
DN BR33:105778

TI **REVIEW** OF EXPERIMENTS USIN **SPERGILLUS-ORYZAE**
FERMENTATION PRODUCTS FOR LACTATING DAIRY COWS.
AU HARRIS B JR
CS UNIV. FLA., GAINESVILLE.
SO 64TH ANNUAL MEETING OF THE AMERICAN DAIRY SCIENCE ASSOCIATION (SOUTHERN BRANCH), NASHVILLE, TENNESSEE, USA, FEBRUARY 1-4, 1987. J DAIRY SCI. (1987) 70 (SUPPL 1), 245.
CODEN: JDSCAE. ISSN: 0022-0302.
DT Conference
FS BR; OLD
LA English

=> FIL STNGUIDE

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	35.26	35.41

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=> s aspergillus oryzae and gene
L9 448 ASPERGILLUS ORYZAE AND GENE

=> s l9 and expression
L10 241 L9 AND EXPRESSION

=> s l9 and express?
L11 284 L9 AND EXPRESS?

=> s l11 and sequence
L12 209 L11 AND SEQUENCE

=> s l12 and py<1998
L13 109 L12 AND PY<1998

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DUPLICATE PREFERENCE IS 'MEDLINE, BIOSIS'
KEEP DUPLICATES FROM MORE THAN ONE FILE? Y/(N):n
PROCESSING COMPLETED FOR L13
L14 68 DUPLICATE REMOVE L13 (41 DUPLICATES REMOVED)

=> d 1-10 bib ab

L14 ANSWER 1 OF 68 MEDLINE DUPLICATE 1
AN 97394941 MEDLINE
DN 97394941 PubMed ID: 9251203
TI Characterization of the **gene** encoding an extracellular laccase of Myceliophthora thermophila and analysis of the recombinant enzyme **expressed** in **Aspergillus oryzae**.
AU Berka R M; Schneider P; Golightly E J; Brown S H; Madden M; Brown K M; Halkier T; Mondorf K; Xu F
CS Novo Nordisk Biotech, Inc., Davis, California, USA.. ramb@novo.dk
SO APPLIED AND ENVIRONMENTAL MICROBIOLOGY, **(1997 Aug)** 63 (8) 3151-7.

Journal code: 6K6; 760580 ISSN: 0099-2240.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-T10922
EM 199709
ED Entered STN: 19970926
Last Updated on STN: 19990129
Entered Medline: 19970918
AB A genomic DNA segment encoding an extracellular laccase was isolated from the thermophilic fungus Myceliophthora thermophila, and the nucleotide **sequence** of this **gene** was determined. The deduced amino acid **sequence** of M. thermophila laccase (MtL) shows homology to laccases from diverse fungal genera. A vector containing the M. thermophila laccase coding region, under transcriptional control of an **Aspergillus oryzae** alpha-amylase **gene** promoter and terminator, was constructed for heterologous **expression** in A. oryzae. The recombinant laccase **expressed** in A. oryzae was purified to electrophoretic homogeneity by anion-exchange chromatography. Amino-terminal **sequence** data suggests that MtL is synthesized as a preproenzyme. The molecular mass was estimated to be approximately 100 to 140 kDa by gel filtration on Sephacryl S-300 and to be 85 kDa by sodium dodecyl sulfate-polyacrylamide gel electrophoresis. Carbohydrate analysis revealed that MtL contains 40 to 60% glycosylation. The laccase shows an absorbance spectrum that is typical of blue copper oxidases, with maxima at 276 and 589 nm, and contains 3.9 copper atoms per subunit. With syringaldazine as a substrate, MtL has optimal activity at pH 6.5 and retains nearly 100% of its activity when incubated at 60 degrees C for 20 min. This is the first report of the cloning and heterologous **expression** of a thermostable laccase.

L14 ANSWER 2 OF 68 MEDLINE DUPLICATE 2
AN 97312003 MEDLINE
DN 97312003 PubMed ID: 9168614
TI Cloning of a protopectinase **gene** of Trichosporon penicillatum and its **expression** in Saccharomyces cerevisiae.
AU Iguchi K; Hirano H; Kishida M; Kawasaki H; Sakai T
CS Department of Applied Biochemistry, College of Agriculture, Osaka Prefecture University, Japan.
SO MICROBIOLOGY, **(1997 May)** 143 (Pt 5) 1657-64.
Journal code: BXW; 9430468. ISSN: 1350-0872.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-D89650
EM 199707
ED Entered STN: 19970805
Last Updated on STN: 19970805
Entered Medline: 19970721
AB A protopectinase (PPase)-encoding **gene**, PSE3, from Trichosporon penicillatum was cloned by colony hybridization using two oligonucleotide probes synthesized from the N-terminal amino acid **sequences** of native PPase SE1 and one peptide from a lysyl endopeptidase digest. Nucleotide sequencing revealed that PSE3 contains an ORF encoding a 367 amino acid protein. Mature PPase SE3 is composed of 340 amino acids and the N-terminus of the ORF appeared to correspond to a signal peptide and a propeptide processed by a KEX2-like proteinase. The deduced amino acid **sequence** of PSE3 was 65.4, 56.7, 58.1, 61.8 and 48.9% homologous to the polygalacturonases of **Aspergillus oryzae**, Aspergillus niger, Aspergillus tubigensis, Cochliobolus carbonum and Fusarium moniliforme, respectively. One domain, which might interact with polygalacturonic acid, is highly conserved not only in fungal polygalacturonases but also in bacterial and plant polygalacturonases. PSE3 was **expressed** in Saccharomyces cerevisiae, but three forms (the mature form, a glycosylated form and an uncharacterized processed form) of PPase SE3 were present among the PSE3 products.

L14 ANSWER 3 OF 68 MEDLINE DUPLICATE 3

AN 97321854 MEDLINE
DN 97321854 PubMed ID: 9178556
TI Efficient **expression** of mono- and diacylglycerol lipase **gene** from Penicillium camembertii U-150 in **Aspergillus oryzae** under the control of its own promoter.
AU Yamaguchi S; Takeuchi K; Mase T; Matsuura A
CS Tsukuba Research Laboratories, Amano Pharmaceutical Co., Ltd., Ibaraki, Japan.
SO BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, **(1997 May)** 61 (5) 800-5.
Journal code: BDP; 9205717. ISSN: 0916-8451.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS B
EM 199707
ED Entered STN: 19970812
Last Updated on STN: 19970812
Entered Medline: 19970731
AB The **gene**, mdlA, coding for mono- and diacylglycerol lipase from Penicillium camembertii U-150 was **expressed** efficiently in **Aspergillus oryzae** under the control of its own promoter. The **gene** product was secreted into the culture medium with a highest productivity of 1 g/liter and correctly processed at both N- and C-termini. KEX2-like processing was suggested to occur at the C-terminus in both A. oryzae and P. camembertii. Specific activity and substrate specificity of the purified recombinant protein were also almost the same to that of native protein but the extent of N-glycosylation in the recombinant protein was about half of that of the native protein. The presence of introns did not seem to affect the **gene expression**. The mdlA **expression** was induced by lipids and regulated transcriptionally in A. oryzae as well as P. camembertii. Promoter deletion analysis showed that the region between the positions at -382 and -554 bp from the translation initiation point was important to the higher **expression** of mdlA. The promoter **sequence** of mdlA was compared to that of the Geotrichum candidum lipase **gene**, which is also reported to be inducible by lipids, with three commonly observed oligonucleotide **sequences**.

L14 ANSWER 4 OF 68 MEDLINE DUPLICATE 4
AN 97270622 MEDLINE
DN 97270622 PubMed ID: 9169610
TI Molecular cloning and heterologous **expression** of the isopullulanase **gene** from Aspergillus niger A.T.C.C. 9642.
AU Aoki H; Yopi; Sakano Y
CS Department of Applied Biological Science, Faculty of Agriculture, Tokyo University of Agriculture and Technology, 3-5-8 Saiwaicho, Fuchu, Tokyo 183, Japan.
SO BIOCHEMICAL JOURNAL, **(1997 May 1)** 323 (Pt 3) 757-64.
Journal code: 9YO; 2984726R. ISSN: 0264-6021.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-D85240
EM 199706
ED Entered STN: 19970716
Last Updated on STN: 19970716
Entered Medline: 19970627
AB Isopullulanase (IPU) from Aspergillus niger A.T.C.C. (American Type Culture Collection) 9642 hydrolyses pullulan to isopanose. IPU is important for the production of isopanose and is used in the structural analysis of oligosaccharides with alpha 1,4 and alpha-1,6 glucosidic linkages. We have isolated the ipuA **gene** encoding IPU from the filamentous fungi A. niger A.T.C.C. 9642. The ipuA **gene** encodes an open reading frame of 1695 bp (564 amino acids). IPU contained a signal **sequence** of 19 amino acids, and the molecular mass of the mature form was calculated to be 59 kDa. IPU has no amino-acid-**sequence** similarity with the other pullulan-hydrolysing enzymes, which are pullulanase, neopullulanase and glucoamylase. However, IPU showed a high

amino-acid-**sequence** similarity with dextranases from Penicillium minioluteum (61%) and Arthrobacter sp. (56%). When the ipuA **gene** was **expressed** in **Aspergillus oryzae**, the **expressed** protein (recombinant IPU) had IPU activity and was immunologically reactive with antibodies raised against native IPU. The substrate specificity, thermostability and pH profile of recombinant IPU were identical with those of the native enzyme, but recombinant IPU (90 kDa) was larger than the native enzyme (69-71 kDa). After deglycosylation with peptide-N-glycosidase F, the deglycosylated recombinant IPU had the same molecular mass as deglycosylated native enzyme (59 kDa). This result suggests that the carbohydrate chain of recombinant IPU differed from that of the native enzyme.

L14 ANSWER 5 OF 68 MEDLINE DUPLICATE 5
AN 97212020 MEDLINE
DN 97212020 PubMed ID: 9058960
TI Cloning, sequencing, and **expression** of a thermostable cellulase **gene** of Humicola grisea.
AU Takashima S; Nakamura A; Masaki H; Uozumi T
CS Department of Biotechnology, Faculty of Agriculture, University of Tokyo, Japan.
SO BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, **(1997 Feb)** 61 (2) 245-50.
Journal code: BDP; 9205717. ISSN: 0916-8451.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS B
OS GENBANK-D84420
EM 199704
ED Entered STN: 19970424
Last Updated on STN: 19990129
Entered Medline: 19970411
AB The egl2 **gene** coding a thermostable endoglucanase (EGL2) was cloned from Humicola grisea. The DNA **sequence** of egl2 predicted two putative introns in the coding region. The deduced amino acid **sequence** of EGL2 was 388 amino acids in length and showed 99.5% identity with the H. insolens CMC 3. In addition to TATA box and CAAT motifs, putative CREA binding sites were observed in the 5' upstream region of the egl2 **gene**. The egl2 **gene** was **expressed** in **Aspergillus oryzae**, and EGL2 was purified. EGL2 produced by A. oryzae showed a high activity toward carboxymethyl cellulose. The optimal temperature of EGL2 was 75 degrees C, and EGL2 had more than 80% residual activity after heating up to 75 degrees C for 10 min. This is the first report of enzymatic properties of the EGL2-type thermostable cellulase homologs from Humicola.

L14 ANSWER 6 OF 68 MEDLINE DUPLICATE 6
AN 1998019092 MEDLINE
DN 98019092 PubMed ID: 9358060
TI Cloning and **sequence** analysis of the **gene** (eprA1) encoding an extracellular protease from Aeromonas hydrophila.
AU Chang T M; Liu C C; Chang M C
CS Department of Biochemistry, Medical College, National Cheng Kung University, Tainan, Taiwan.
SO GENE, **(1997 Oct 15)** 199 (1-2) 225-9.
Journal code: EOP; 7706761. ISSN: 0378-1119
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-U93600
EM 199711
ED Entered STN: 19971224
Last Updated on STN: 20000303
Entered Medline: 19971124
AB A **gene** (eprA1) encoding the extracellular protease of Aeromonas hydrophila AH1 has been cloned and sequenced. Nucleotide **sequence** analysis of eprA1 predicted a single open reading frame (ORF) of 1038 bp encoding a 346 amino acid (aa) polypeptide, with a potential 21-aa signal

peptide. When the eprA1 g[redacted] was **expressed** in minicells, one major band of approx. 37 kDa was identified, while protease activity staining experiments identified a caseinolytic band of approx. 29 kDa determined by SDS-PAGE analysis of the minicells. The deduced C-terminal aa region (Arg-290 to Gly-313) showed **sequence** homology to partial C-terminal **sequences** of other zinc metalloproteases including Penicillium citrinum metalloprotease (PlnC), **Aspergillus oryzae** metalloprotease (NpII), Aspergillus flavus metalloprotease (MepA), and Aspergillus fumigatus metalloprotease (Mep20), particularly with respect to zinc-binding residues.

L14 ANSWER 7 OF 68 MEDLINE
AN 97444510 MEDLINE
DN 97444510 PubMed ID: 9299700
TI **Expression** cloning of fungal enzyme **genes**; a novel approach for efficient isolation of enzyme **genes** of industrial relevance.
AU Dalboge H
CS Enzyme Business. Novo Nordisk AIS, Bagsvard, Denmark.. hda@novo.dk
SO FEMS MICROBIOLOGY REVIEWS, **(1997 Aug)** 21 (1) 29-42. Ref: 21
Journal code: AO4; 8902526. ISSN: 0168 6445.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199710
ED Entered STN: 19971013
Last Updated on STN: 19971013
Entered Medline: 19971001
AB **Expression** cloning is a relatively new method for fast and efficient cloning of enzyme **genes** from fungi that are known to make complex enzyme mixtures. In contrast to traditional cloning methods that are usually dependent on knowledge of at least a partial amino acid **sequence** in order to synthesize appropriate DNA probes or primers, the **expression** cloning method solely relies on access to reliable and sensitive enzyme assays. A representative **expression** cDNA library is made in Saccharomyces cerevisiae form the donor strain and relevant cDNA clones are detected directly based on the encoded enzyme activity. Thus, time-consuming enzyme purification and characterization steps are avoided. The method has been applied on the characterization of extracellular enzyme **genes** from the filamentous fungus Aspergillus aculeatus and has resulted in the isolation of 20 different enzyme **genes** such as endo-glucanases, xylanases, pectinases, proteases, hemicellulases and rhamnogalacturonan-degrading enzymes. All enzymes have been **expressed** in **Aspergillus oryzae**, purified and characterized. In the present review a description of the **expression** cloning technique will be given as well as examples of how the technique has been used in the exploration and characterization of a commercial enzyme product that is known to consist of a complex mixture of more than 25 different enzyme activities.

L14 ANSWER 8 OF 68 MEDLINE DUPLICATE 7
AN 97141594 MEDLINE
DN 97141594 PubMed ID: 8987852
TI **Sequence**-specific binding sites in the Taka-amylase A G2 promoter for the CreA repressor mediating carbon catabolite repression.
AU Kato M; Sekine K; Tsukagoshi N
CS Department of Applied Biological Sciences, Faculty of Agriculture, Nagoya University, Japan.
SO BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, **(1996 Nov)** 60 (11) 1776-9.
Journal code: BDP; 9205717. ISSN: 0916-8451.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS B
EM 199702
ED Entered STN: 19970306

Last Updated on STN: 1997[redacted]6
Entered Medline: 19970224
AB The N-terminal part of the CreA protein encompassing two zinc fingers was **expressed** in Escherichia coli as a fusion protein with the maltose binding protein (MalE) of E. coli. Our results show that CreA binds to the promoter of the Taa-G2 **gene** encoding Taka-amylase A of **Aspergillus oryzae**. DNase I footprinting experiments showed that CreA bound to three sites with high affinity and to one site with low affinity within the first 401-bp region upstream of the transcription initiation site. All of the sites contained **sequences** related to the CreA consensus binding site (5'-SYGGRG-3'), and are suggested to participate in repression of the Taa-G2 **gene** in response to glucose.

L14 ANSWER 9 OF 68 MEDLINE DUPLICATE 8
AN 97076915 MEDLINE
DN 97076915 PubMed ID: 8975613
TI Purification, characterization, molecular cloning, and **expression** of two laccase **genes** from the white rot basidiomycete Trametes villosa.
AU Yaver D S; Xu F; Golightly E J; Brown K M; Brown S H; Rey M W; Schneider P; Halkier T; Mondorf K; Dalboge H
CS Novo Nordisk Biotech, Davis, California 95616, USA.
SO APPLIED AND ENVIRONMENTAL MICROBIOLOGY, **(1996 Mar)** 62 (3) 834-41.
Journal code: 6K6; 7605801. ISSN: 0099-2240.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-L49376; GENBANK-L49377
EM 199612
ED Entered STN: 19970128
Last Updated on STN: 19990129
Entered Medline: 19961231
AB Two laccases have been purified to apparent electrophoretic homogeneity from the extracellular medium of a 2,5-xylidine-induced culture of the white rot basidiomycete Trametes villosa (Polyporus pinsitus or Coriolus pinsitus). These proteins are dimeric, consisting of two subunits of 63 kDa as determined by sodium dodecyl sulfate-polyacrylamide gel electrophoresis, and have typical blue laccase spectral properties. Under nondenaturing conditions, the two purified laccases have different pIs; purified laccase forms 1 and 3 have pIs of 3.5 and 6 to 6.5, respectively. A third purified laccase form 2 has the same N terminus as that of laccase form 3, but its pI is in the range of 5 to 6. The laccases have optimal activity at pH 5 to 5.5 and pH < or = 2.7 with syringaldazine and ABTS [2,2'-azinobis-(3-ethylbenzthiazoline-6-sulfonic acid)] as substrates, respectively. The **genes** lcc1 and lcc2 coding for the two purified laccases (forms 1 and 3) have been cloned, and their nucleotide **sequences** have been determined. The **genes** for lcc1 and lcc2 have 8 and 10 introns, respectively. The predicted proteins are 79% identical at the amino acid level. From Northern (RNA) blots containing total RNA from both induced and uninduced cultures, **expression** of lcc1 is highly induced, while the **expression** of lcc2 appears to be constitutive. Lcc1 has been **expressed** in **Aspergillus oryzae**, and the purified recombinant protein has the same pI, spectral properties, stability, and pH profiles as the purified native protein.

L14 ANSWER 10 OF 68 MEDLINE
AN 97161783 MEDLINE
DN 97161783 PubMed ID: 9008887
TI Molecular cloning, purification and characterization of two endo-1,4-beta-glucanases from **Aspergillus oryzae** KBN616.
AU Kitamoto N; Go M; Shibayama T; Kimura T; Kito Y; Ohmiya K; Tsukagoshi N
CS Food Research Institute, Aichi Prefectural Government, Nagoya, Japan.
SO APPLIED MICROBIOLOGY AND BIOTECHNOLOGY, **(1996 Dec)** 46 (5-6) 538-44.
Journal code: AMC; 8406612. ISSN: 0175-7598.

CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS B
OS GENBANK-D83731; GENBANK-D83732
EM 199703
ED Entered STN: 19970313
    Last Updated on STN: 19970313
    Entered Medline: 19970305
AB Two endo-1,4-beta-glucanase **genes**, designated celA and celB,
    from a shoyu koji mold **Aspergillus oryzae** KBN616, were
    cloned and characterized. The celA **gene** comprised 877 bp with
    two introns. The CelA protein consisted of 239 amino acids and was
    assigned to the cellulase family H. The celB **gene** comprised 1248
    bp with no introns. The CelB protein consisted of 416 amino acids and was
    assigned to the cellulase family C. Both **genes** were
    overexpressed under the promoter of the A. oryzae taka-amylase A
    gene for purification and enzymatic characterization of CelA and
    CelB. CelA had a molecular mass of 31 kDa, a pH optimum of 5.0 and
    temperature optimum of 55 degrees C, whereas CelB had a molecular mass of
    53 kDa, a pH optimum of 4.0 and temperature optimum of 45 degrees C.

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    (FILE 'HOME' ENTERED AT 16:16:52 ON 13 FEB 2002)

    FILE 'MEDLINE, BIOSIS' ENTERED AT 16:17:17 ON 13 FEB 2002
L1   6 S ORYZAE AND ARRAY
L2   6 DUPLICATE REMOVE L1 (0 DUPLICATES REMOVED)
L3   2 S ASPERGILLUS ORYZAE AND ARRAY
L4   2 DUPLICATE REMOVE L3 (0 DUPLICATES REMOVED)
L5   660 S ASPERGILLUS ORYZAE AND (GENE OR SEQUENCE OR CDNA)
L6   24 S ASPERGILLUS ORYZAE AND REVIEW
L7   17 S L6 AND PY<1998
L8   16 DUPLICATE REMOVE L7 (1 DUPLICATE REMOVED)

    FILE 'STNGUIDE' ENTERED AT 16:24:26 ON 13 FEB 2002

    FILE 'MEDLINE, BIOSIS' ENTERED AT 16:27:03 ON 13 FEB 2002
L9   448 S ASPERGILLUS ORYZAE AND GENE
L10   241 S L9 AND EXPRESSION
L11   284 S L9 AND EXPRESS?
L12   209 S L11 AND SEQUENCE
L13   109 S L12 AND PY<1998
L14   68 DUPLICATE REMOVE L13 (41 DUPLICATES REMOVED)

=> s l14 not expressed in
L15   36 L14 NOT EXPRESSED IN

=> d 1-10 bib ab

L15 ANSWER 1 OF 36   MEDLINE
AN   97161783   MEDLINE
DN   97161783   PubMed ID: 9008887
TI   Molecular cloning, purification and characterization of two
     endo-1,4-beta-glucanases from **Aspergillus oryzae**
     KBN616.
AU   Kitamoto N; Go M; Shibayama T; Kimura T; Kito Y; Ohmiya K; Tsukagoshi N
CS   Food Research Institute, Aichi Prefectural Government, Nagoya, Japan.
SO   APPLIED MICROBIOLOGY AND BIOTECHNOLOGY, **(1996 Dec)** 46 (5-6)
     538-44.
     Journal code: AMC; 8406612. ISSN: 0175-7598.
CY   GERMANY: Germany, Federal Republic of
DT   Journal; Article; (JOURNAL ARTICLE)
LA   English
FS   B
OS   GENBANK-D83731; GENBANK-D83732
EM   199703
ED   Entered STN: 19970313

Last Updated on STN: 19970
Entered Medline: 19970305

AB Two endo-1,4-beta-glucanase **genes**, designated celA and celB, from a shoyu koji mold **Aspergillus oryzae** KBN616, were cloned and characterized. The celA **gene** comprised 877 bp with two introns. The CelA protein consisted of 239 amino acids and was assigned to the cellulase family H. The celB **gene** comprised 1248 bp with no introns. The CelB protein consisted of 416 amino acids and was assigned to the cellulase family C. Both **genes** were overexpressed under the promoter of the A. oryzae taka-amylase A **gene** for purification and enzymatic characterization of CelA and CelB. CelA had a molecular mass of 31 kDa, a pH optimum of 5.0 and temperature optimum of 55 degrees C, whereas CelB had a molecular mass of 53 kDa, a pH optimum of 4.0 and temperature optimum of 45 degrees C.

L15 ANSWER 2 OF 36 MEDLINE
AN 97074675 MEDLINE
DN 97074675 PubMed ID: 8917102
TI Cloning and sequencing of the **gene** encoding tannase and a structural study of the tannase subunit from **Aspergillus oryzae**.
CM Erratum in: Gene 1997 Feb 20;186(1):153
AU Hatamoto O; Watarai T; Kikuchi M; Mizusawa K; Sekine H
CS Noda Institute for Scientific Research, Chiba, Japan.
SO GENE, **(1996 Oct 10)** 175 (1-2) 215-21.
Journal code: FOP; 7706761. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-D63338
EM 199612
ED Entered STN: 19970128
Last Updated on STN: 19980206
Entered Medline: 19961216

AB We cloned the **Aspergillus oryzae** tannase **gene** using three oligodeoxyribonucleotide (oligo) probes synthesized according to the tannase N-terminal and an internal amino acid (aa) **sequence**. The nucleotide (nt) **sequence** of the tannase **gene** was determined and compared with that of a tannase DNA complementary to RNA (cDNA) by means of reverse transcriptase PCR. The results indicated that there was no intron in the tannase **gene** and that it coded for 588 aa with a molecular weight of about 64,000. The tannase low-producing strain A. oryzae AO1 was transformed with the plasmid pT1 which contained the tannase **gene**, and tannase activities of the transformants increased in proportion to the number of copies. Tannase consisted of two kinds of subunits, linked by a disulfide bond(s) with molecular weights of about 30,000 and 33,000, respectively. We purified these subunits and determined their N-terminal aa **sequences**. The large and small subunits of tannase were encoded by the first and second halves, respectively. Judging from the above results, the tannase **gene** product is translated as a single polypeptide that is cleaved by post-translational modification into two tannase subunits linked by a disulfide bond(s). We concluded that native tannase consisted of four pairs of the two subunits, forming a hetero-octamer with a molecular weight of about 300,000.

L15 ANSWER 3 OF 36 MEDLINE
AN 97074235 MEDLINE
DN 97074235 PubMed ID: 8929396
TI Deletion analysis of promoter elements of the **Aspergillus oryzae** agdA **gene** encoding alpha glucosidase.
AU Minetoki T; Nunokawa Y; Gomi K; Kitamoto K; Kumagai C; Tamura G
CS General Research Laboratory, Ozeki Corp., 4-9, Imazu Dezaike cho, Nishinomiya-shi, Hyogo 663, Japan.
SO CURRENT GENETICS, **(1996 Nov)** 30 (5) 432-8.
Journal code: CUG; 8004904. ISSN: 0172-8083.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English

FS Priority Journals
OS GENBANK-D45179
EM 199702
ED Entered STN: 19970305
Last Updated on STN: 19970305
Entered Medline: 19970220
AB The nucleotide **sequence** of a 1.5-kb fragment of the promoter region of the **Aspergillus oryzae** agdA **gene** encoding alpha-glucosidase was determined. A comparison with the promoter regions of other Aspergillus amylase **genes** indicated that there are three highly conserved **sequences**, designated Regions I, II and III, located at -670 nt, -596 nt and -544 nt relative to the start codon, respectively. The function of these consensus **sequences** in the agdA promoter was investigated by deletion analysis of a promoter fusion with the Escherichia coli uidA **gene**, using the niaD homologous-transformation system. Deletion of the upstream half of Region III (IIIa; -544 to -529) resulted in a more than 90% reduction in GUS activity and abolished maltose induction, suggesting that Region IIIa is a functionally essential element for high-level **expression** and maltose induction. Deletion of Region I and the downstream half of Region III (IIIb; -521 to -511) resulted in a significant reduction in GUS activity, but did not affect maltose induction. This suggested that these two elements most likely contain **sequences** involved in efficient **expression** in cooperation with Region IIIa. In addition, deletion of a 340-bp region between Region IIIb and the putative TATA box resulted in a 2-fold increase in activity.

L15 ANSWER 4 OF 36 MEDLINE
AN 97074234 MEDLINE
DN 97074234 PubMed ID: 8929395
TI Molecular cloning of a cDNA encoding enolase from the filamentous fungus, **Aspergillus oryzae**.
AU Machida M; Chang Y C; Manabe M; Yasukawa M; Kunihiro S; Jigami Y
CS Department of Molecular Biology, National Institute of Bioscience and Human-Technology, Higashi 1-1, Tsukuba, Ibaraki 305, Japan.
SO CURRENT GENETICS, **(1996 Nov)** 30 (5) 423-31.
Journal code: CUG; 8004904. ISSN: 0172-8083.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199702
ED Entered STN: 19970305
Last Updated on STN: 19970305
Entered Medline: 19970220
AB A 1.6-kbp full-length cDNA for the **Aspergillus oryzae** enolase **gene** (enoA) was cloned. The sequenced insert contained a continuous open reading frame of 1314 bp encoding a protein of molecular weight 47 405. Among all enolases sequenced to-date, the deduced amino acid **sequence** showed the highest homology (74.9%) with Candida albicans enolase (ENO1). Strong codon biases and multiple transcription start sites downstream from CT-blocks in the 5'-flanking region suggested strong **expression**. enoA mRNA was found to occupy approximately 3% (w/w) of total mRNA of A. oryzae by quantitative RT-PCR. This strong transcription was dependent on the carbon source in the medium and correlated with the growth rate of the mycelium.

L15 ANSWER 5 OF 36 MEDLINE
AN 97056756 MEDLINE
DN 97056756 PubMed ID: 8901095
TI Construction of a promoter probe vector autonomously maintained in Aspergillus and characterization of promoter regions derived from A. niger and A. oryzae genomes.
AU Ozeki K; Kanda A; Hamachi M; Nunokawa Y
CS General Research Laboratory, Ozeki Corporation, Hyogo, Japan.
SO BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, **(1996 Mar)** 60 (3) 383-9.
Journal code: BDP; 9205717. ISSN: 0916-8451.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)

LA English
FS B
EM 199612
ED Entered STN: 19970128
Last Updated on STN: 19970128
Entered Medline: 19961226
AB We used a plasmid carrying a **sequence** for autonomous maintenance in Aspergillus (AMA1) and the E. coli uidA **gene** as a reporter **gene** to search the A. oryzae and A. niger genomes for DNA fragments having strong promoter activity. Beta-glucuronidase (GUS)-producing A. oryzae transformants containing the No. 8AN derived from A. niger, or the No. 9AO derived from A. oryzae, were constitutive for the **expression** of the uidA **gene** when cultivated in the presence of a variety of carbon and nitrogen sources. When the GUS-producing transformants were grown in liquid culture, the No. 8AN showed an increase of approximately 3-fold in GUS activity compared to the amyB (alpha-amylase encoding **gene**) promoter. There was also a corresponding increase in the amount of GUS **gene**-specific mRNA. When these transformants were grown as rice-koji, the No. 8AN showed an increase of approximately 6-fold compared to the amyB promoter, and the amount of GUS protein produced also increased. These strong promoter regions might be applicable to the production of other heterologous proteins in Aspergillus species.

L15 ANSWER 6 OF 36 MEDLINE
AN 96422222 MEDLINE
DN 96422222 PubMed ID: 8824839
TI Molecular cloning of a genomic DNA for enolase from **Aspergillus oryzae**.
AU Machida M; Gonzalez T V; Boon L K; Gomi K; Jigami Y
CS Department of Molecular Biology, National Institute of Bioscience and Human-Technology, Ibaraki, Japan.
SO BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, **(1996 Jan)** 60 (1) 161-3.
Journal code: BDP; 9205717. ISSN: 0916-8451.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS B
OS GENBANK-D63941
EM 199703
ED Entered STN: 19970313
Last Updated on STN: 19980206
Entered Medline: 19970306
AB We have isolated an enolase **gene** (enoA) from **Aspergillus oryzae** by heterologous hybridization using the corresponding Saccharomyces cerevisiae ENO2 **gene** as a probe. A 2.9-kb BglII-fragment contained the entire structural **gene** enoA including 5'- and 3'- flanking regions. The homology between A. oryzae enoA and S. cerevisiae ENO2 **genes** is 66.9% when introns are removed. Genomic Southern analysis indicated that there is only one enolase **gene** in A. oryzae.

L15 ANSWER 7 OF 36 MEDLINE
AN 96070823 MEDLINE
DN 96070823 PubMed ID: 7592973
TI Molecular cloning and characterization of a rhamnogalacturonan acetylesterase from Aspergillus aculeatus. Synergism between rhamnogalacturonan degrading enzymes.
AU Kauppinen S; Christgau S; Kofod L V; Halkier T; Dorreich K; Dalboge H
CS GeneSearch, Novo Nordisk A/S, Novo Alle, Bagsvaerd, Denmark.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, **(1995 Nov 10)** 270 (45) 27172-8.
Journal code: HIV; 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-X89714
EM 199512
ED Entered STN: 19960124

Last Updated on STN: 1996[redacted]
Entered Medline: 19951226

AB A rhamnogalacturonan acetylesterase (RGAE) was purified to homogeneity from the filamentous fungus Aspergillus aculeatus, and the NH2-terminal amino acid **sequence** was determined. Full-length cDNAs encoding the enzyme were isolated from an A. aculeatus cDNA library using a polymerase chain reaction-generated product as a probe. The 936-base pair rha1 cDNA encodes a 250-residue precursor protein of 26,350 Da, including a 17-amino acid signal peptide. The rha1 cDNA was overexpressed in **Aspergillus oryzae**, a filamentous fungus that does not possess RGAE activity, and the recombinant enzyme was purified and characterized. Mass spectrometry of the native and recombinant RGAE revealed that the enzymes are heterogeneously glycosylated. In addition, the observed differences in their molecular masses, lectin binding patterns, and monosaccharide compositions indicate that the glycan moieties on the two enzymes are structurally different. The RGAE was shown to act in synergy with rhamnogalacturonase A as well as rhamnogalacturonase B from A. aculeatus in the degradation of apple pectin rhamnogalacturonan. RNA gel blot analyses indicate that the **expression** of rhamnogalacturonan degrading enzymes by A. acculeatus is regulated at the level of transcription and is subjected to carbon catabolite repression by glucose.

L15 ANSWER 8 OF 36 MEDLINE
AN 96068932 MEDLINE
DN 96068932 PubMed ID: 8534978
TI Cloning and nucleotide **sequence** of the ribonuclease T1 **gene** (rntA) from **Aspergillus oryzae** and its **expression** in Saccharomyces cerevisiae and **Aspergillus oryzae**.
AU Fujii T; Yamaoka H; Gomi K; Kitamoto K; Kumagai C
CS National Research Institute of Brewing, Tokyo, Japan.
SO BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, **(1995 Oct)** 59 (10) 1869-74.
Journal code: BDP; 9205717. ISSN: 0916-8451.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS B
OS GENBANK-D28341; GENBANK-D49428
EM 199602
ED Entered STN: 19960221
Last Updated on STN: 19960221
Entered Medline: 19960208

AB A genomic DNA encoding ribonuclease (RNase) T1 from **Aspergillus oryzae** was cloned using a synthetic oligonucleotide probe. The cloned **gene** (designated rntA) encoded functional RNase T1, since an A. oryzae transformant with multiple copies of the rntA **gene** showed higher RNase T1 activity (over 200 times) than a transformant with a vector. A cDNA was cloned by reverse transcription polymerase chain reaction (RT-PCR) with primers corresponding to the 5' terminus and 3' terminus of the reading frame of the rntA **gene**. Nucleotide sequencing analysis of both DNAs found that RNase T1 had a prepro-**sequence** consisting of 26 amino acids and the rntA **gene** had only one intron (114 bp) in the region encoding the signal **sequence**. The A. oryzae transformant with cDNA controlled by the amyB promoter also showed higher activity (over 300 times), indicating that the cloned cDNA encoded functional RNase T1. On the other hand, the Saccharomyces cerevisiae transformant with cDNA controlled by the GAL1 promoter could not grow on a medium containing galactose. These results suggests that A. oryzae may have a protection mechanism from RNase T1.

L15 ANSWER 9 OF 36 MEDLINE
AN 96032211 MEDLINE
DN 96032211 PubMed ID: 7549103
TI Nucleotide **sequence** and **expression** of alpha-glucosidase-encoding **gene** (agdA) from **Aspergillus oryzae**.
AU Minetoki T; Gomi K; Kitamoto K; Kumagai C; Tamura G
CS Research Institute of Brewing Resouces Co., Ltd., Tokyo, Japan.

SO BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, **(1995 Aug)** 59 1516-21.
Journal code: BDP; 9205717. ISSN: 0916-8451.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS B
OS GENBANK-D45179
EM 199511
ED Entered STN: 19951227
Last Updated on STN: 19951227
Entered Medline: 19951106
AB We have isolated an alpha-glucosidase(AGL)-encoding **gene** (agdA) from **Aspergillus oryzae** by heterologous hybridization using the corresponding Aspergillus niger **gene** as a probe. Southern hybridization analysis showed that the agdA **gene** is on a 5.0-kb ScaI fragment and there is a single copy in the A. oryzae chromosome. Comparison with the A. niger agdA **gene** indicated that the agdA **gene** contains three putative introns from 52 to 59 nucleotides long, and that it encodes 985 amino acid residues. The deduced amino acid **sequence** of A. oryzae AGL is 78% homologous with the A. niger AGL. The high degree of homology with the amino acid **sequence** bordering the putative catalytic residue of a number of AGL enzymes, and this enzyme suggests that Asp492 is a catalytic residue of A. oryzae AGL. The cloned **gene** was functional. Transformants of A. oryzae containing multiple copies of the cloned agdA **gene** showed a 6-16 fold increase in AGL activity. Like the Taka-amylase A and glucoamylase **genes** of A. oryzae, **expression** of the agdA **gene** was induced when maltose was provided as a carbon source, but **expression** was not induced by glucose. This result suggested that cis-element(s) involved in maltose induction may be also present in the agdA promoter region.

L15 ANSWER 10 OF 36 MEDLINE
AN 95078777 MEDLINE
DN 95078777 PubMed ID: 7987261
TI **Expression** cloning, purification and characterization of a beta-1,4-mannanase from Aspergillus aculeatus.
AU Christgau S; Kauppinen S; Vind J; Kofod L V; Dalboge H
CS GeneExpress, Novo Nordisk A/S, Copenhagen, Denmark.
SO BIOCHEMISTRY AND MOLECULAR BIOLOGY INTERNATIONAL, **(1994 Aug)** 33 (5) 917-25.
Journal code: BOD; 9306673. ISSN: 1039-9712.
CY Australia
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-L35487
EM 199501
ED Entered STN: 19950124
Last Updated on STN: 19970203
Entered Medline: 19950112
AB A cDNA library from the filamentous fungus Aspergillus aculeatus was constructed in the yeast **expression** vector pYES2.0 and used to isolate 57 full length cDNA's encoding beta-1,4-mannanase by **expression** in S. cerevisiae. The positive clones were identified on agar plates containing 0.2% azurine dyed cross-linked mannan by the formation of blue halos around the colonies. All clones represented transcripts of the same mannanase **gene** (man1). The **gene** was sub-cloned into an Aspergillus **expression** vector and transformed into **Aspergillus oryzae** for overexpression and purification of the enzyme. The recombinant enzyme had a molecular weight of 45 kDa, an isoelectric point of pH 4.5, a pH optimum of pH 5.0 and a temperature optimum of 60-70 degrees.

=> d 11-20 bib ab

L15 ANSWER 11 OF 36 MEDLINE
AN 94368822 MEDLINE

DN 94368822 PubMed ID: 8086[redacted]
TI Elucidation of the thermal stability of the neutral proteinase II from **Aspergillus oryzae**.
AU Tatsumi H; Ikegaya K; Murakami S; Kawabe H; Nakano E; Motai H
CS Research and Development Division, Kikkoman Corporation, Chiba, Japan.
SO BIOCHIMICA ET BIOPHYSICA ACTA, **(1994 Sep 21)** 1208 (1) 179-85.
Journal code: A0W; 0217513. ISSN: 0006-3002.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199410
ED Entered STN: 19941031
Last Updated on STN: 20000303
Entered Medline: 19941018
AB The neutral proteinase II from **Aspergillus oryzae** (NpII) is a zinc proteinase with three intramolecular disulfide bonds. NpII is most unstable after 10 min at about 75 degrees C, but regains stability beyond this temperature and is relatively stable at 100 degrees C. We analyzed the thermal stability of wild-type NpII and apo NpII. The results suggested that NpII unfolds reversibly upon incubation up to 100 degrees C, and that the irreversible inactivation observed is mainly due to autoproteolysis. To further understand the stability, a mutant NpII (Cys78-->Ala) lacking one of the disulfide bonds, was produced in a heterologous yeast **expression** system. The mutant NpII showed a similar stability profile, but the most unstable temperature and the most catalytically active temperature decreased to the same extent (around 10 degrees C), confirming that autoproteolysis is the main cause of the irreversible inactivation. Several lines of evidence presented in this study demonstrated that the thermal stability of o++NpII is attributed to reversible thermal unfolding and autoproteolysis.

L15 ANSWER 12 OF 36 MEDLINE
AN 94264394 MEDLINE
DN 94264394 PubMed ID: 7764853
TI Cloning and nucleotide **sequence** of the alkaline protease **gene** from Fusarium sp. S-19-5 and **expression** in Saccharomyces cerevisiae.
AU Morita S; Kuriyama M; Maejima K; Kitano K
CS Discovery Research Laboratories, Takeda Chemical Industries, Ltd., Osaka, Japan.
SO BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, **(1994 Apr)** 58 (4) 621-6.
Journal code: BDP; 9205717. ISSN: 0916-8451.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS B
EM 199407
ED Entered STN: 19950809
Last Updated on STN: 20000303
Entered Medline: 19940712
AB We have cloned a genomic DNA encoding the alkaline protease (Alp) of Fusarium sp. S-19-5 from a genomic DNA library and sequenced the nucleotides. Complementary DNA encoding Alp was also isolated from the cDNA library after amplifying the **gene** by PCR using partial **sequences** of the Alp genomic DNA as primers. The Alp **gene** has an open reading frame of 1137 nucleotides containing three introns. A TATA box (TAAATA) was observed 112 base pairs upstream from the translation initiation codon in the 5'-non coding region. The Alp protein has a pre region consisting of 14 amino acids and a pro region of 85 amino acids preceding the mature region, which consists of 280 amino acids. The amino acid **sequence** of Fusarium Alp has 52% homology with that of **Aspergillus oryzae** and 51% homology with that of Acremonium chrysogenum. The entire cDNA encoding Fusarium Alp was introduced into Saccharomyces cerevisiae, which then secreted enzymatically active Alp into the culture medium.

L15 ANSWER 13 OF 36 MEDLINE
AN 94010226 MEDLINE

DN 94010226 PubMed ID: 8405[redacted]
TI **Expression** of **Aspergillus oryzae** alpha-amylase **gene** in Saccharomyces cerevisiae.
AU Randez-Gil F; Sanz P
CS Instituto de Agroquimica y Tecnologia de los Alimentos (C.S.I.C.), Valencia, Spain.
SO FEMS MICROBIOLOGY LETTERS, **(1993 Aug 15)** 112 (1) 119-23.
Journal code: FML; 7705721. ISSN: 0378-1097.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199311
ED Entered STN: 19940117
Last Updated on STN: 19940117
Entered Medline: 19931110
AB A fragment containing the full length cDNA from **Aspergillus oryzae** alpha-amylase has been amplified by PCR using specific synthetic oligonucleotides. The amplified cDNA was designed to favour its **expression** in yeast by modifying its upstream untranslated region. It was subcloned in the **expression** vector pYEX alpha 1, placed under the control of the yeast CYC1-GAL10 promoter and used to transform Saccharomyces cerevisiae. Cells were then able to **express** and secrete active alpha-amylase to the medium in a regulated fashion. The recombinant enzyme had similar electrophoretic mobility and catalytic properties to the original A. oryzae alpha-amylase.

L15 ANSWER 14 OF 36 MEDLINE
AN 93372482 MEDLINE
DN 93372482 PubMed ID: 7763981
TI Cloning and nucleotide **sequence** of the acid protease-encoding **gene** (pepA) from **Aspergillus oryzae**.
AU Gomi K; Arikawa K; Kamiya N; Kitamoto K; Kumagai C
CS National Research Institute of Brewing, Tokyo, Japan.
SO BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, **(1993 Jul)** 57 (7) 1095-100.
Journal code: BDP; 9205717. ISSN: 0916-8451.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS B
OS GENBANK-D13894
EM 199310
ED Entered STN: 19950809
Last Updated on STN: 20000303
Entered Medline: 19931004
AB We have cloned a genomic DNA **sequence** encoding the acid protease (PEPA) from **Aspergillus oryzae** using a 0.6-kb fragment as a probe. This fragment was amplified by the polymerase chain reaction (PCR) using oligonucleotide primers designed from the partial amino acid **sequences** of peptide fragments of the purified protein. Nucleotide sequencing analysis has shown that the cloned **gene** (designated pepA) encodes 404 amino acid residues and contains 3 putative introns ranging in length from 50 to 61 nucleotides. The deduced amino acid **sequence** of the A. oryzae PEPA has a high degree of homology (67%) to the A. awamori PEPA. Comparison with the amino acid **sequence** of A. awamori PEPA suggests that the A. oryzae PEPA may consist of a 78 amino acid prepro peptide and 326 amino acid mature protein. The amino acid composition of the mature protein was almost consistent with that of the acid protease purified from A. oryzae reported previously. Southern hybridization analyses showed that the pepA **gene** exists as a single copy in the A. oryzae chromosome. The cloned **gene** was found to be functional, since transformants of A. oryzae containing multiple copies of the pepA **gene** showed a 2-6 fold increase in acid protease activity compared with the recipient strain.

L15 ANSWER 15 OF 36 MEDLINE
AN 93204901 MEDLINE
DN 93204901 PubMed ID: 8455560
TI Aspergillus nidulans nuclear proteins bind to a CCAAT element and the

adjacent upstream **sequence** in the promoter region of the starch-inducible Taka-amylase A **gene**.
AU Nagata O; Takashima T; Tanaka M; Tsukagoshi N
CS Department of Food Science and Technology, Faculty of Agriculture, Nagoya University, Japan.
SO MOLECULAR AND GENERAL GENETICS, **(1993 Feb)** 237 (1-2) 251-60.
Journal code: NGP; 0125036. ISSN: 0026-8925.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199304
ED Entered STN: 19930507
Last Updated on STN: 19930507
Entered Medline: 19930416
AB Aspergillus nidulans was used as an intermediate host to investigate the regulation of the Taka-amylase A (TAA) **gene** from **Aspergillus oryzae**. The induction of Taa by starch was confirmed to be regulated at the transcriptional level by analyzing the transcripts specific for Taa synthesized in vitro in nuclei from starch- and glucose-grown cells. A 55 bp DNA fragment containing a consensus CCAAT **sequence** from the promoter region of the Taa **gene** was shown to confer starch inducibility on the **gene**. A nuclear extract from starch-grown cells was assayed for proteins which bind to the promoter region of the Taa **gene**. A protein designated AnCP1 bound to the CCAAT **sequence**. A nuclear extract from glucose-grown cells contained two DNA-binding proteins designated AnCP2 and AnNP1. AnCP2 bound to the same CCAAT **sequence** as AnCP1, while AnNP1 bound to the 25 bp region just upstream of the AnCP2 binding site. Occupancy of the two binding sites appeared to be mutually exclusive, which is suggestive of a negative regulatory mechanism for **gene expression**.

L15 ANSWER 16 OF 36 MEDLINE
AN 93192006 MEDLINE
DN 93192006 PubMed ID: 7763442
TI Production of a fungal protein, Taka-amylase A, by protein-producing Bacillus brevis HPD31.
AU Ebisu S; Mori M; Takagi H; Kadowaki K; Yamagata H; Tsukagoshi N; Udaka S
CS Research Laboratory, Higeta Shoyu Co., Ltd., Chiba, Japan.
SO JOURNAL OF INDUSTRIAL MICROBIOLOGY, **(1993 Feb)** 11 (2) 83-8.
Journal code: ALF; 8610887. ISSN: 0169-4146.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS B
EM 199304
ED Entered STN: 19950809
Last Updated on STN: 19950809
Entered Medline: 19930409
AB An **expression**-secretion vector, pMK300, was constructed to **express** the **Aspergillus oryzae** Taka-amylase A (Taa) cDNA. The promoter and signal peptide regions of the HWP (a major cell wall protein of Bacillus brevis HPD31) **gene** on pMK300 were efficiently utilized in B. brevis HPD31 and a large amount of Taa (22 mg/l) was secreted into the medium. The HWP signal peptide utilized for secretion of Taa was correctly processed during the protein transport across the membrane. The enzymatic properties of Taa produced by B. brevis HPD31 were the same as those of the **Aspergillus oryzae** Taa in several respects; specific activity, thermal and pH stabilities, and temperature and pH optima. These results, in combination with previous results, indicate that B. brevis HPD31 could be used to produce extracellularly foreign proteins of diverse origins as functional proteins.

L15 ANSWER 17 OF 36 MEDLINE
AN 93113093 MEDLINE
DN 93113093 PubMed ID: 1369079
TI Deletion analysis of the Taka-amylase A **gene** promoter using a homologous transformation system in **Aspergillus oryzae**

AU Tsuchiya K; Tada S; Gomi K; Kitamoto K; Kumagai C; Tamura G
CS Research Institute of Brewing Resources Co., Ltd., Tokyo, Japan.
SO BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, **(1992 Nov)** 56 (11) 1849-53.
Journal code: BDP; 9205717. ISSN: 0916-8451.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS B
EM 199302
ED Entered STN: 19950809
Last Updated on STN: 19950809
Entered Medline: 19930203
AB The Taka-amylase A **gene** (amyB) of **Aspergillus oryzae** is induced by starch or maltose. The molecular mechanism of the induction was investigated using a fusion of the amyB promoter and the Escherichia coli uidA **gene** encoding beta-glucuronidase (GUS). To identify the region responsible for high-level **expression** and regulation within the amyB promoter, a series of deletion promoters was constructed and introduced into the A. oryzae met locus by homologous recombination. Deletion of the region between -377 to -290 (the number indicates the distance in base pairs from the translation initiation point (+1) to the deletion end point) significantly reduced of the GUS activity, but slight reduction of the GUS activity was observed in deletions up to -377. Northern blot analysis showed that reduction of the GUS activity depended upon the **expression** level of the GUS **gene**. The region between -377 to -290 is suggested to include the **sequence** required directly for high-level **expression** and regulation of the amyB **gene**.

L15 ANSWER 18 OF 36 MEDLINE
AN 93113077 MEDLINE
DN 93113077 PubMed ID: 1369066
TI Overproduction of an alpha-amylase/glucoamylase fusion protein in **Aspergillus oryzae** using a high **expression** vector.
AU Shibuya I; Tsuchiya K; Tamura G; Ishikawa T; Hara S
CS Research Institute, Brewing Resources Co., Ltd., Tokyo, Japan.
SO BIOSCIENCE, BIOTECHNOLOGY, AND BIOCHEMISTRY, **(1992 Oct)** 56 (10) 1674-5.
Journal code: BDP; 9205717. ISSN: 0916-8451.
CY Japan
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS B
EM 199302
ED Entered STN: 19950809
Last Updated on STN: 19950809
Entered Medline: 19930202

L15 ANSWER 19 OF 36 MEDLINE
AN 93046803 MEDLINE
DN 93046803 PubMed ID: 1339327
TI Functional elements of the promoter region of the **Aspergillus oryzae** glaA **gene** encoding glucoamylase.
AU Hata Y; Kitamoto K; Gomi K; Kumagai C; Tamura G
CS Research Institute of Brewing Resources Co., Ltd., Tokyo, Japan.
SO CURRENT GENETICS, **(1992 Aug)** 22 (2) 85-91.
Journal code: CUG; 8004904. ISSN: 0172-8083.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-M81727; GENBANK-M81728; GENBANK-M81754; GENBANK-S72771; GENBANK-X65481; GENBANK-X65482; GENBANK-X67419; GENBANK-Z11730; GENBANK-Z11731; GENBANK-Z11733
EM 199212
ED Entered STN: 19930122
Last Updated on STN: 19930122

Entered Medline: 19921211

AB Analysis was made of the promoter region of the **Aspergillus oryzae** glaA **gene** encoding glucoamylase. Northern blots using a glucoamylase cDNA as a probe indicated that the amount of mRNA corresponding to the glaA **gene** increased when **expression** was induced by starch or maltose. The promoter region of the glaA **gene** was fused to the Escherichia coli uidA **gene**, encoding beta-glucuronidase (GUS), and the resultant plasmid was introduced into A. oryzae. **Expression** of GUS protein in the A. oryzae transformants was induced by maltose, indicating that the glaA-GUS **gene** was regulated at the level of transcription in the presence of maltose. The nucleotide **sequence** 1.1 kb upstream of the glaA coding region was determined. A comparison of the nucleotide **sequence** of the A. oryzae glaA promoter with those of A. oryzae amyB, encoding alpha-amylase, and A. niger glaA showed two regions with similar **sequences**. Deletion and site-specific mutation analysis of these homologous regions indicated that both are essential for direct high-level **expression** when grown on maltose.

L15 ANSWER 20 OF 36 MEDLINE
AN 92175518 MEDLINE
DN 92175518 PubMed ID: 1541396
TI The Aspergillus niger niaD **gene** encoding nitrate reductase: upstream nucleotide and amino acid **sequence** comparisons.
AU Unkles S E; Campbell E I; Punt P J; Hawker K L; Contreras R; Hawkins A R; Van den Hondel C A; Kinghorn J R
CS Plant Molecular Genetics Unit, University of St. Andrews, Fife, U.K.
SO GENE, **(1992 Feb 15)** 111 (2) 149-55.
Journal code: FOP; 7706761. ISSN: 0378-1119.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-M64367; GENBANK-M64425; GENBANK-M64426; GENBANK-M64427; GENBANK-M77022; GENBANK-S39996; GENBANK-S40001; GENBANK-S40008; GENBANK-S40009; GENBANK-S40010
EM 199204
ED Entered STN: 19920424
Last Updated on STN: 19920424
Entered Medline: 19920408
AB The Aspergillus niger niaD **gene** has been sequenced and the inferred nitrate reductase (NR) protein found to consist of 867 amino acid residues (97 kDa). The **gene** is interrupted by six small introns, as deduced by comparison with the niaD **gene** of Aspergillus nidulans. The positions of these putative introns are conserved between the two fungi, although the **sequences** are dissimilar. The niiA **gene**, encoding nitrite reductase, the second reductive step in the nitrate assimilation pathway, is tightly linked to niaD and divergently transcribed in A. niger, similar to the general organisation in the related fungi, **Aspergillus oryzae** and A. nidulans. The nucleotide (nt) **sequences** of the intergenic region between niiA and niaD (excluding the ATG translation start codon) of A. niger (1668 nt) and A. oryzae (1575 nt) were determined and compared with the previously determined A. nidulans (1262 nt) **sequence**. No striking extended nt regions of homology are observed in spite of the fact that transgenic strains with fungal niaD or the two control **genes** required for induction and repression show virtually normal regulation. Fungal NR shows considerable aa homology with higher plant NR, particularly within the co-factor domains for flavin adenoside dinucleotide, heme and molybdopterin cofactor.

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---Logging off of STN---

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Executing the logoff script...

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COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	18.07	53.48

STN INTERNATIONAL LOGOFF AT 16:39:54 ON 13 FEB 2002

Connection closed by remote host